OM nucleic - nucleic search, using sw model

```
                    GenCore version 5.1.7
          Copyright (c) 1993 - 2006 Bioacceleration Ltd.
```

Run on: April 18, 2006, 07:49:48 ; Search time 1.01497 Seconds
                                            (without alignments)
                                            3.508 Million cell updates/sec

Title: US-10-646-950-5
Perfect score: 373
Sequence: 1 tttgggagtccgcccatttca.........gcctcagagaccctactgtg 373

Scoring table:
                IDENTITY_NUC
                Gapop 10.0 , Gapext 0.5

Searched: 2 seqs, 4773 residues

Total number of hits satisfying chosen parameters: 4

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 2 summaries

Database :   US10646950_1_3.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

```
                              SUMMARIES

Result                    %    Query
  No.   Score  Match  Length  DB  ID          Description
  1     30.5   8.2    2948    1   US-10-646-950-3   Sequence 3, Appli
  2     16.4   4.4    1825    1   US-10-646-950-1   Sequence 1, Appli
```

                              ALIGNMENTS

RESULT 1
US-10-646-950-3
; Sequence 3, Application US/10646950
; GENERAL INFORMATION:
; APPLICANT: Rine, Jasper
; APPLICANT: Boyartchuk, Victor L
; APPLICANT: Ashby, Matthew N
; TITLE OF INVENTION: AFC1 and RCE1: Isoprenylated CAAX Processing Enzymes
; FILE REFERENCE: B96-021-3
; CURRENT APPLICATION NUMBER: US/10/646,950
; CURRENT FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: 60/023,491
; PRIOR FILING DATE: 1996-08-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3
; LENGTH: 2948
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1001)..(1945)
US-10-646-950-3

Query Match   8.2%;   Score 30.5; DB 1; Length 2948;
Best Local Similarity   49.8%; Pred. No. 0;

```
Qy  178  TTCTGCAACTACATGGGGCTTCCCTG  202
         |||||  ||||  ||  ||  ||  |||
Db  1748 CTTTGCAATATACATGGGGGTTTCCTG  1772
```

(and further alignment blocks)

RESULT 2
US-10-646-950-1
; Sequence 1, Application US/10646950
; GENERAL INFORMATION:
; APPLICANT: Rine, Jasper
; APPLICANT: Boyartchuk, Victor L
; APPLICANT: Ashby, Matthew N
; TITLE OF INVENTION: AFC1 and RCE1: Isoprenylated CAAX Processing Enzymes
; FILE REFERENCE: B96-021-3
; CURRENT APPLICATION NUMBER: US/10/646,950
; CURRENT FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: 60/023,491
; PRIOR FILING DATE: 1996-08-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1825
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (343)..(1701)
US-10-646-950-1

Query Match   4.4%;   Score 16.4; DB 1; Length 1825;
Best Local Similarity   45.4%; Pred. No. 0;
Matches   59; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

```
Qy   98  ACACCGCTGTCTTCGGTGCTTATACAGCTTTCCTCTTCATCCGCACAGGACACCTGATAG  157
         ||  | || ||  |  || |    ||||| || ||||   ||||| |  |  || | ||
Db  356  AGACGGATTCTCGACCATCCTAATATCCGTGGAAATTAATCATTTCTCGGTTCTCGATTG  415

Qy  158  GGCCGGTTCTCTGCCACTCTCTTTCTGCAACTACATGGGCTTCCCTGCAGTGTGTGCAGCCC  217
         ||||| |||  || ||  |   ||| |  |  ||||| ||  |||  ||| | ||| | ||
Db  416  CCCAATTTTCTTTCGAATCTTACTTGACGTACAGAGACAGTACCAGAGAGCTATCTGAAACAA  475

Qy  218  TGGAGGCATCC  227
         ||  ||  |||
Db  476  AGTTGCCACC  485
```

Search completed: April 18, 2006, 07:49:50
Job time : 1.01497 secs

```
                    GenCore version 5.1.7
          Copyright (c) 1993 - 2006 Bioacceleration Ltd.
```

OM nucleic - nucleic search, using sw model

Run on: April 18, 2006, 07:49:48 ; Search time 0.985034 Seconds
                                            (without alignments)
                                            3.508 Million cell updates/sec

Title:
Perfect score: 358
Sequence: US-10-646-950-6
Sequence: 1 cattattacaagatgaatt...........gagagacttcaagcttcgaa 362

Scoring table: IDENTITY_NUC
                  Gapop 10.0 , Gapext 0.5

Searched: 2.seqs, 4773 residues

Total number of hits satisfying chosen parameters: 4

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 2 summaries

Database :   US10646950_1_3.seq:*

SUMMARIES

Result
No.   Score   %   Query
               Match Length DB ID   Description
------ ----- ------ ------ -- --   -----------
  1   33.7   9.4   1825   1   US-10-646-950-1   Sequence 1, Appli
c 2   24.4   6.8   2948   1   US-10-646-950-3   Sequence 3, Appli

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

ALIGNMENTS

RESULT 1
US-10-646-950-1
Sequence 1, Application US/10646950
GENERAL INFORMATION:
;   APPLICANT: Rine, Jasper
;   APPLICANT: Boyartchuk, Victor L
;   APPLICANT: Ashby, Matthew N
;   TITLE OF INVENTION: AFC1 and RCE1: Isoprenylated CAAX Processing Enzymes
;   FILE REFERENCE: B96-021-3
;   CURRENT APPLICATION NUMBER: US/10/646,950
;   CURRENT FILING DATE: 2003-08-21
;   PRIOR APPLICATION NUMBER: 60/023,491
;   PRIOR FILING DATE: 1996-08-07
;   NUMBER OF SEQ ID NOS: 6
;   SOFTWARE: PatentIn Ver. 2.1
;
;   SEQ ID NO 1
;   LENGTH: 1825
;   TYPE: DNA
;   ORGANISM: Saccharomyces cerevisiae
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (343)..(1701)
US-10-646-950-1

Query Match   9.4%; Score 33.7; DB 1; Length 1825;
Best Local Similarity   55.2%; Pred. No. 0;
Matches 85; Conservative   0; Mismatches 68; Indels   1; Gaps   1;

Qy   196 TGAGTTTCAAGCTGATGCAT-TGCCAAGAAAACTTGGGAAGGCTAAAGACTTATATTCTGC 254
              |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db   1509 TGAATATCAAGCTGATGCTTATGCTAAAAAAATTGGGCTACAAGCAAAAATCTATGTAGGGC 1568

Qy   255 TTTAATCAAACTTAACAAAGATAACTTGGGATTCCCTGTTTCTGACTTGTGTTCTCAAT 314
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1569 TCTAATTGATCTACAAAAATCAAAAAACCTTTCCACCATGAAAGTAGATCCTCTGTATTCTAG 1628

Qy   315 GTGGCATTATTCTCATCCTCCACTGCTAGAGAGA 348

RESULT 2
US-10-646-950-3/c
Sequence 3, Application US/10646950
GENERAL INFORMATION:
;   APPLICANT: Rine, Jasper
;   APPLICANT: Boyartchuk, Victor L
;   APPLICANT: Ashby, Matthew N
;   TITLE OF INVENTION: AFC1 and RCE1: Isoprenylated CAAX Processing Enzymes
;   FILE REFERENCE: B96-021-3
;   CURRENT APPLICATION NUMBER: US/10/646,950
;   CURRENT FILING DATE: 2003-08-21
;   PRIOR APPLICATION NUMBER: 60/023,491
;   PRIOR FILING DATE: 1996-08-07
;   NUMBER OF SEQ ID NOS: 6
;   SOFTWARE: PatentIn Ver. 2.1
;
;   SEQ ID NO 3
;   LENGTH: 2948
;   TYPE: DNA
;   ORGANISM: Saccharomyces cerevisiae
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1001)..(1945)
US-10-646-950-3

Query Match   6.8%; Score 24.4; DB 1; Length 2948;
Best Local Similarity   46.7%; Pred. No. 0;
Matches 70; Conservative   0; Mismatches 80; Indels   0; Gaps   0;

Qy   27 TGTGTTTTTTTTTTTTATTTGCTGTATTAATTGGTCGAAAGGAGCTTTTTTTTGCTTGGTT 86
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2862 TATATTTTGTAAAGTATCTTGTACAAGCTCTAGGAAAATTATCAGGCTTAACGTTAGGGTG 2803

Qy   87 TTTATGNTAGCCAACCCACTNTATTGGACTANTGNTCATCTTCCAGTTATTTTTTTCAC 146
              |||| |||| ||| ||| ||| ||| || || | |||| |||||||||| ||
Db   2802 TTGATTGGCGGGAACCCATAATAAGTTTTTCTTTAATACGTTAGCATTAAATTCCTGGA 2743

Qy   147 CTTACAATGNGGTTCTTTCTTTCTTTTTGCCTAA 176
              |||||||||||||||||||||||||||||||||
Db   2742 TCGAGAGTGAACACCTTTTTTTTATACCTAA 2713

Db   1629 CTATCATTATTCCCATCCAACTCTAGCTGAAAGA 1662

From:	Ramirez, Delia
Sent:	Monday, April 10, 2006 1:36 PM
To:	Jarrell, Noble
Subject:	10/646950

Hi,
I would like to request the following alignments:

1. SEQ ID NO:5 against SEQ ID NO:2 and 4
2. SEQ ID NO:6 against SEQ ID NO:2 and 4
3. SEQ ID NO:5 against SEQ ID NO:6
4. SEQ ID NO:5 and 6 against SEQ ID NO:1
5. SEQ ID NO:5 and 6 against SEQ ID NO:3
6. SEQ ID NO:1 and 3 against SEQ ID NO:2 and 4

Thank you very much,

Delia M. Ramirez, Ph.D.
Patent Examiner
Recombinant Enzymes-Art Unit 1652
USPTO
400 Dulany Street, Remsen Bldg., 2D74, Mail room 2C70
Alexandria, VA 22314
(571) 272-0938
delia.ramirez@uspto.gov

1

Best Local Similarity: 36.4%   Mismatches: 39
Query Match: 9.9%   Indels: 6
DB: 1   Gaps: 3

US-10-646-950-4 (1-315) x US-10-646-950-5 (1-373)

```
Qy 190 PheGlyLeuValAlaHisAlaHisHisAlaAlaTyrGluGlnLeuGlnHisGlySerMetThrThr 209
       |||||||  |||                                      :::
Db   1 TTTGGAGTCGCCCATTTTACCACATTATTGAGCAGCTGCA                        ::: 
Qy 210 ValSerIleLeuLeuThrThrCysPheGlnIleLeuTyrThrThrLeuPheGlyLeu 229
       |||||||||||  |                                  :::
Db  61 GGAAGTATCTTCGTGTCTCGAGCGGTTCCAGTTCCTACACCGCGTCTTCGGTGCTTAT 120
Qy 230 ThrLysPheValPheValArgThrGlyGlyAsnLeuLeuTrpLeuValThrGlyGlyAsnLeuAla 249
       |||||||                                          :::::
Db 121 ACAGCTTTCCTCTTCATCCGCACA--GGACACTGATAGGGCGCGGTTCATCGCCACTCA 177
Qy 250 LeuCysAsnIleMetGlyPheProGlyProSerArgLeuAsnLeuHisPheThrValVal 269
       ::::                                             :::::
Db 178 TTCTGCAACTACAAGGGCTTCCCTGGACCCTGGAGCAT 225
Qy 270 AspLysLysAlaGlyArgIleSerLeuValSerIleTrpAsn---LysCysTyr 287
       |||                                              :::
Db 226 CCACAGAGTGGGCCACTGCTGGCAGGCTATGCCTCGGTGTGGGGGACTTTTCCTGCTTC 282
```

RESULT 3
US-10-646-950-1
Sequence 1, Application US/10646950
GENERAL INFORMATION:
APPLICANT: Rine, Jasper
APPLICANT: Boyartchuk, Victor L
APPLICANT: Ashby, Matthew N
TITLE OF INVENTION: AFC1 and RCE1: Isoprenylated CAAX Processing Enzymes
FILE REFERENCE: B96-021-3
CURRENT APPLICATION NUMBER: US/10/646,950
CURRENT FILING DATE: 2003-08-21
PRIOR APPLICATION NUMBER: 60/023,491
PRIOR FILING DATE: 1996-08-07
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 1825
TYPE: DNA
ORGANISM: Saccharomyces cerevisiae
FEATURE:
NAME/KEY: CDS
LOCATION: (343)..(1701)

US-10-646-950-1

Alignment Scores:
Pred. No.:
Score: 2.86
Percent Similarity: 54.00   Length: 1825
Best Local Similarity: 37.7%   Matches: 75
Query Match: 24.6%   Conservative: 40
DB: 3.3%   Mismatches: 112
     Indels: 80
     Gaps: 15

US-10-646-950-4 (1-315) x US-10-646-950-1 (1-1825)

```
Qy   2 LeuGlnPheSerThrPheLeuValLeuLeuTyr------IleSerIleSerTyrVal 18
       ||||| |||||||  ||||||||||                :::SerTyrVal
Db   1 TTAAACTTTTCCCTCTTTTTCTAGGTCATCAAAAAACTCTAATTCCTTCGTTCTCTG 18
Qy  19 LeuProLeuTyrAlaThrSerGlnProGluGly------SerLysArgAspAsnProArg 36
       |:|                                    :::
Db 130 TTCTGCCATTTTCTCCAGAAAAAATCGACGGGAAATAAAAAAAAGCAACGAACAA 189
Qy  37 ------ThrIleLysSerArgMetGln 43
       :::
Db 190 TTCTGCCATTTTCTCCAGAAAAAATCGACGGGAAATAAAAAAAAGCAACGAACAA 249
Qy  44 LysLeuThrIleMetLeuIleSerAsnLeuPheLeuValProPheLeuGlnSerGlnLeu 63
       :::
Db 250 GAGAAAAAAGTTCCGGAATTATAAAACCACTTCTATATAATTAACAGGAAAAGGAAGGAAAAAAA 309
```

RESULT 4
US-10-646-950-3/c
Sequence 3, Application US/10646950
GENERAL INFORMATION:
APPLICANT: Rine, Jasper
APPLICANT: Boyartchuk, Victor L
APPLICANT: Ashby, Matthew N
TITLE OF INVENTION: AFC1 and RCE1: Isoprenylated CAAX Processing Enzymes
FILE REFERENCE: B96-021-3
CURRENT APPLICATION NUMBER: US/10/646,950
CURRENT FILING DATE: 2003-08-21
PRIOR APPLICATION NUMBER: 60/023,491
PRIOR FILING DATE: 1996-08-07
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3
LENGTH: 2948
TYPE: DNA
ORGANISM: Saccharomyces cerevisiae
FEATURE:
NAME/KEY: CDS
LOCATION: (1001)..(1945)

```
Db 310 AAGGAGGAGAAATAGAGAAAACTGCAGGCCTTTATTCATGTTT 354
       |||                                    |||||||||:::
Qy  64 SerSerThrThrSerHis------IleSerPheLys-AspAlaPheLeuGlyIleLeuGlyIl 81
       :::                                    |||||||||
Db 355 AAGACAGATTCTCGACCATTCCTTAATATCCCGTGGAAATTAATCATTTCTGGGT 406
Qy  81 eIleProGlyTyrTyrAlaAlaLeuProAsnProTrpGlnPheSerGlnPheValLysAs 101
       |||                                    :::
Db 407 ------------------TCTCGATTGCCCAAT------- 432
Qy 101 pLeu------------ThrLysCysValAlaMetLeuLeuThrLeuTyrCysGlyProValIle 118
       |||                                    :::
Db 433 TCTTACTTGACGTACAGACAGACTACCAGAGCTATCTGAAACAAAAGTTGCCA--CCTGTGCT 491
Qy 118 uAspPheValLeu------TyrHisLeuAsnPr 128
       :::
Db 492 GGAACAGCGAAATTGATGATGAAACTTTTCATATAAAAATCAAGGAGGGGCCAAGGC 551
Qy 128 oGlySerSerIleLeuGluAspPheTyrHisGluPheLeuAsnIleTrpSerProRgAs 148
       :::                                    |||
Db 552 CAAGTTCTCCATTTTCCGTGACGTCTAT------AACCTTAGCCCAAAAGCTAGT 599
Qy 148 nPheIlePheAlaProIleThrGlyIleuIlePheTyrThrSerMetLeuLeuThrThrTy 168
       |||                                    |||
Db 600 TTTCATCAAATACGACCTCTTCCCCTAAAAATCTGGCACATGGCCGGTTTCTTTA------ 651
Qy 168 rLeuAsnLeuIleProHisSerGlnLeuSerTyrGlnGlnLeuPheTrpGlnProSerIle 188
       :::                                    |||:::
Db 652 -TTGAATGCAGT-CCTGCCAGTCAGATTTCATAT------ 683
Qy 188 uPhePheGlyLeuValAlaHisAlaHisAlaAlaTyrGluGlnLeuGlnLeuGlySer-MetT 208
       :::                                    |||
Db 684 ------GGTCTC---CACTGTCGCACAGAGTTTAATCGTTCTTGGGTTCTCTTAT 727
Qy 208 hrThrValSerIleLeuLeuThrThrCysPheGlnIleLeuLeuTyrThrThrLeuPheGlyG 228
       :::                                    |||:::
Db 728 CCAGTTGTCTACCCTTGGGTTGAT------TTGCCACTCTCTTACTATAGGCCATTTTGTCC 781
Qy 228 lyLeuThrLysPheValPheValArgThrGlyGlyAsnLeuLeuTrpLeuValThrGlyGlyAsnLeuLeuH 248
       :::                                    |||
Db 782 TGGAAGAAAAATTTGGTTTCAATAAAATTGACCGTCCAACTATATGGGATCAACACCGGATATGATCA 841
Qy 248 isAlaLeuCysAsnIleMetGlyPheProGlyProSerArgLeuAsnLeuAsnLeuHisPheThrV 268
       :::                                    |||
Db 842 AGAGTCTGACTTTGGCGTATGCTATTGGGTGGCCCAAATC---CTTTACCTGTTCCTTAAGA 898
Qy 268 alValAspLys 271
       ||||||
Db 899 TCTTTGATAAA 909
```

```
US-10-646-950-3

Alignment Scores:
Pred. No.:
Score:                  3.17                    Length:            2948
Percent Similarity:     43.50                   Matches:           45
Best Local Similarity:  37.5%                   Conservative:      27
Query Match:            23.4%                    Mismatches:        65
DB:                     2.6%                     Indels:            56
                        1                        Gaps:              10

US-10-646-950-4 (1-315) x US-10-646-950-3 (1-2948)

Qy     80 GlyIleIleProGlyTyr------------------------TyrAlaAlaLeuProAsn 91
          |||||||||::||||                           ||::|||||::::
Db   1903 GGTAttCCTTCAGGGATATTAAATCCAAAGGACCAGAGTGCGAAGTAGCACTTATTCCAGAT 1844

Qy     92 ProTrpGlnPhe-----------SerGln-PheValLysAspLeuThrLysCysValAlaMe 108
          ||||||                 |||||:|
Db   1843 TGAGACCAAATTTGGAAAATGCGTCCAGCTTTCTTGTCTACTACTGTGAAATGTAAATTCAA 1784

Qy    108 tLeuLeuThrLeuTyrCysGlyTyrProValLeuAspPheValLeuTyrHisLeuLeuAsnPr 128
          ||||                                  ||::|||
Db   1783 TCTTTGAA-------------------------GGACCAGGAAACCCCATGATATTGCAAAGGGCATGCAGG-- 1738

Qy    128 oLySSerSerIleLeuGluAspPheTyrHisGluPheLeuAsnIleTrpSerPheArgAs 148
          |||::|::::                            :::
Db   1737 ----------ATTATGCAG-----CACCATAGGTTCCCGCCTGTTCTTACGAATTACAAA 1694

Qy    148 nPheIleProIleThrGluGlu-IlePheTyrThrSerMetLeuLeuThrThrT 168
          :::|||||                         ||||||||||
Db   1693 CTTGGTTAACCCTCCAAAAAGTTGTTGTATAAAATTTGGAAGCATGTTG------ 1644

Qy    168 yrIleuAsnLeuIleProHisSerGlnLeuSerTyrGlnGlnLeuPheTrpGlnProSerL 188
          :::|||:|||||                      |:||||
Db   1643 --------------------------TCAGCAGAATGGAAACAGTTGTCATGGAGCCTTCCTG 1607

Qy    188 euPhePheGlyLeuAlaHisAlaHisHisAlaTyrGluGlnLeuGlnGlySerMetT 208
          :::|||||                       ||:|||||||
Db   1606 TA-------AATTGCTCATAAGCATGTGTGCGTGCCCAAGTCCAAAAAAAGCGATGG 1556

Qy    208 hr--------------------------ThrValSerIleLeuLeuThr----------- 215
          |||:::
Db   1555 TTGCCAAAATAACTGTTGATAGCGTTAGTTGCGAATGCGTATTAGGTTTAAGTACGTAGT 1496

Qy    216 -----------ThrCysPheGlnIleLeuThrLeuPheGlyLeuThrLysP 232
          |||||||                        ||||
Db   1495 CAAAAGCATTGACGTGTAA-AATATT-----TCCTCAGTTATTGGGTGCAAATATAAAAT 1443

Qy    232 heValPheValArgThrGlyGlyAsnLeuTrp 242
          |||:|::         ::::|
Db   1442 TCCTGAAACTCCAAATATTCAGGAATTCATGG 1411
```

Search completed: April 18, 2006, 07:40:36
Job time : 2.64062 secs

OM nucleic - nucleic search, using sw model

Copyright (c) 1993 - 2006   GenCore version 5.1.7
Bioacceleration Ltd.

Run on: April 18, 2006, 07:54:24 ; Search time 0.001 Seconds
(without alignments)
270.052 Million cell updates/sec

Title: US-10-646-950-5
Perfect Score: 373
Sequence: 1 tttggagtcgcgcccatttca.........gcctcagagacctactgtg 373

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 362 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1 summaries

Database :   Pending_Patents_NA_Main:US-10-646-950-6

```
 1: /cgn2_6/ptodata/1/pna/PCTUSA_COMB.seq:US-10-646-950-6
 2: /cgn2_6/ptodata/1/pna/PCTUSB_COMB.seq:US-10-646-950-6
 3: /cgn2_6/ptodata/1/pna/PCTUSC_COMB.seq:US-10-646-950-6
 4: /cgn2_6/ptodata/1/pna/US06_COMB.seq:US-10-646-950-6
 5: /cgn2_6/ptodata/1/pna/US075_COMB.seq:US-10-646-950-6
 6: /cgn2_6/ptodata/1/pna/US076_COMB.seq:US-10-646-950-6
 7: /cgn2_6/ptodata/1/pna/US077_COMB.seq:US-10-646-950-6
 8: /cgn2_6/ptodata/1/pna/US078_COMB.seq:US-10-646-950-6
 9: /cgn2_6/ptodata/1/pna/US079_COMB.seq:US-10-646-950-6
10: /cgn2_6/ptodata/1/pna/US080_COMB.seq:US-10-646-950-6
11: /cgn2_6/ptodata/1/pna/US081_COMB.seq:US-10-646-950-6
12: /cgn2_6/ptodata/1/pna/US082_COMB.seq:US-10-646-950-6
13: /cgn2_6/ptodata/1/pna/US083_COMB.seq:US-10-646-950-6
14: /cgn2_6/ptodata/1/pna/US084_COMB.seq:US-10-646-950-6
15: /cgn2_6/ptodata/1/pna/US085_COMB.seq:US-10-646-950-6
16: /cgn2_6/ptodata/1/pna/US086_COMB.seq:US-10-646-950-6
17: /cgn2_6/ptodata/1/pna/US087_COMB.seq:US-10-646-950-6
18: /cgn2_6/ptodata/1/pna/US088_COMB.seq:US-10-646-950-6
19: /cgn2_6/ptodata/1/pna/US089_COMB.seq:US-10-646-950-6
20: /cgn2_6/ptodata/1/pna/US090_COMB.seq:US-10-646-950-6
21: /cgn2_6/ptodata/1/pna/US091_COMB.seq:US-10-646-950-6
22: /cgn2_6/ptodata/1/pna/US092_COMB.seq:US-10-646-950-6
23: /cgn2_6/ptodata/1/pna/US093_COMB.seq:US-10-646-950-6
24: /cgn2_6/ptodata/1/pna/US094_COMB.seq:US-10-646-950-6
25: /cgn2_6/ptodata/1/pna/US095A_COMB.seq:US-10-646-950-6
26: /cgn2_6/ptodata/1/pna/US095B_COMB.seq:US-10-646-950-6
27: /cgn2_6/ptodata/1/pna/US095C_COMB.seq:US-10-646-950-6
28: /cgn2_6/ptodata/1/pna/US096A_COMB.seq:US-10-646-950-6
29: /cgn2_6/ptodata/1/pna/US096B_COMB.seq:US-10-646-950-6
30: /cgn2_6/ptodata/1/pna/US096C_COMB.seq:US-10-646-950-6
31: /cgn2_6/ptodata/1/pna/US097A_COMB.seq:US-10-646-950-6
32: /cgn2_6/ptodata/1/pna/US097B_COMB.seq:US-10-646-950-6
33: /cgn2_6/ptodata/1/pna/US098A_COMB.seq:US-10-646-950-6
34: /cgn2_6/ptodata/1/pna/US098B_COMB.seq:US-10-646-950-6
35: /cgn2_6/ptodata/1/pna/US099A_COMB.seq:US-10-646-950-6
36: /cgn2_6/ptodata/1/pna/US099B_COMB.seq:US-10-646-950-6
37: /cgn2_6/ptodata/1/pna/US099C_COMB.seq:US-10-646-950-6
38: /cgn2_6/ptodata/1/pna/US099D_COMB.seq:US-10-646-950-6
39: /cgn2_6/ptodata/1/pna/US099E_COMB.seq:US-10-646-950-6
40: /cgn2_6/ptodata/1/pna/US100A_COMB.seq:US-10-646-950-6
41: /cgn2_6/ptodata/1/pna/US100B_COMB.seq:US-10-646-950-6
42: /cgn2_6/ptodata/1/pna/US101_COMB.seq:US-10-646-950-6
43: /cgn2_6/ptodata/1/pna/US102A_COMB.seq:US-10-646-950-6
44: /cgn2_6/ptodata/1/pna/US102B_COMB.seq:US-10-646-950-6
45: /cgn2_6/ptodata/1/pna/US103A_COMB.seq:US-10-646-950-6
46: /cgn2_6/ptodata/1/pna/US103B_COMB.seq:US-10-646-950-6
47: /cgn2_6/ptodata/1/pna/US103C_COMB.seq:US-10-646-950-6
48: /cgn2_6/ptodata/1/pna/US103D_COMB.seq:US-10-646-950-6
49: /cgn2_6/ptodata/1/pna/US103E_COMB.seq:US-10-646-950-6
50: /cgn2_6/ptodata/1/pna/US103F_COMB.seq:US-10-646-950-6
51: /cgn2_6/ptodata/1/pna/US104_COMB.seq:US-10-646-950-6
52: /cgn2_6/ptodata/1/pna/US105_COMB.seq:US-10-646-950-6
53: /cgn2_6/ptodata/1/pna/US106A_COMB.seq:US-10-646-950-6
54: /cgn2_6/ptodata/1/pna/US106B_COMB.seq:US-10-646-950-6
55: /cgn2_6/ptodata/1/pna/US107A_COMB.seq:US-10-646-950-6
56: /cgn2_6/ptodata/1/pna/US107B_COMB.seq:US-10-646-950-6
57: /cgn2_6/ptodata/1/pna/US107C_COMB.seq:US-10-646-950-6
58: /cgn2_6/ptodata/1/pna/US107D_COMB.seq:US-10-646-950-6
59: /cgn2_6/ptodata/1/pna/US107E_COMB.seq:US-10-646-950-6
60: /cgn2_6/ptodata/1/pna/US107F_COMB.seq:US-10-646-950-6
61: /cgn2_6/ptodata/1/pna/US107G_COMB.seq:US-10-646-950-6
62: /cgn2_6/ptodata/1/pna/US108_COMB.seq:US-10-646-950-6
63: /cgn2_6/ptodata/1/pna/US109A_COMB.seq:US-10-646-950-6
64: /cgn2_6/ptodata/1/pna/US109B_COMB.seq:US-10-646-950-6
65: /cgn2_6/ptodata/1/pna/US109C_COMB.seq:US-10-646-950-6
66: /cgn2_6/ptodata/1/pna/US110A_COMB.seq:US-10-646-950-6
67: /cgn2_6/ptodata/1/pna/US110B_COMB.seq:US-10-646-950-6
68: /cgn2_6/ptodata/1/pna/US110C_COMB.seq:US-10-646-950-6
69: /cgn2_6/ptodata/1/pna/US110D_COMB.seq:US-10-646-950-6
70: /cgn2_6/ptodata/1/pna/US111A_COMB.seq:US-10-646-950-6
71: /cgn2_6/ptodata/1/pna/US111B_COMB.seq:US-10-646-950-6
72: /cgn2_6/ptodata/1/pna/US112_COMB.seq:US-10-646-950-6
73: /cgn2_6/ptodata/1/pna/US117_COMB.seq:US-10-646-950-6
74: /cgn2_6/ptodata/1/pna/US600_COMB.seq:US-10-646-950-6
75: /cgn2_6/ptodata/1/pna/US601_COMB.seq:US-10-646-950-6
76: /cgn2_6/ptodata/1/pna/US602A_COMB.seq:US-10-646-950-6
77: /cgn2_6/ptodata/1/pna/US602B_COMB.seq:US-10-646-950-6
78: /cgn2_6/ptodata/1/pna/US603_COMB.seq:US-10-646-950-6
79: /cgn2_6/ptodata/1/pna/US604A_COMB.seq:US-10-646-950-6
80: /cgn2_6/ptodata/1/pna/US604B_COMB.seq:US-10-646-950-6
81: /cgn2_6/ptodata/1/pna/US605_COMB.seq:US-10-646-950-6
82: /cgn2_6/ptodata/1/pna/US606_COMB.seq:US-10-646-950-6
83: /cgn2_6/ptodata/1/pna/US607_COMB.seq:US-10-646-950-6
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB ID	Description
1	13.6	3.6	362	54	US-10-646-950-6 Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-10-646-950-6
Sequence 6, Application US/10646950
GENERAL INFORMATION:
; APPLICANT: Rine, Jasper
; APPLICANT: Boyartchuk, Victor L
; APPLICANT: Ashby, Matthew N
; TITLE OF INVENTION: AFC1 and RCE1: Isoprenylated CAAX Processing Enzymes
; FILE REFERENCE: B96-021-3
; CURRENT APPLICATION NUMBER: US/10/646,950
; CURRENT FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: 60/023,491
; PRIOR FILING DATE: 1996-08-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 362

```
;   TYPE: DNA
;   ORGANISM: human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (93)..(156)
;   OTHER INFORMATION: "n" is G, A, C or T
US-10-646-950-6

Query Match        3.6%;    Score 13.6;   DB 54;   Length 362;
Best Local Similarity    61.1%;    Pred. No. 0;
Matches   22;   Conservative    0;   Mismatches   14;   Indels    0;   Gaps    0;

Qy     277 TGCTTCTGCTTCAACCCCTGACACGACCCCAAGCTCT 312
               ||||||  ||||   | |||||||   |||||||||
Db     324 TTCTCATCCTCCACTGCTAGAGAGAGACTTCAAGCTTT 359

Search completed: April 18, 2006, 07:54:28
Job time : 1 secs
```

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 18, 2006, 07:49:48 ; Search time 1.01497 Seconds
                                            (without alignments)
                                            3.508 Million cell updates/sec

Title: US-10-646-950-5
Perfect score: 373
Sequence: 1 tttggagtcgcgccatttca.........gcctcagagaccctactgtg 373

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 0.5

Searched: 2 seqs, 4773 residues

Total number of hits satisfying chosen parameters: 4

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 2 summaries

Database :   US10646950_1_3.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	Query Match Length	DB	ID	Description
1	30.5	8.2	2948	1	US-10-646-950-3	Sequence 3, Appli
2	16.4	4.4	1825	1	US-10-646-950-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-10-646-950-3
Sequence 3, Application US/10646950
; GENERAL INFORMATION:
; APPLICANT: Rine, Jasper
; APPLICANT: Boyartchuk, Victor L
; APPLICANT: Ashby, Matthew N
; TITLE OF INVENTION: AFC1 and RCE1: Isoprenylated CAAX Processing Enzymes
; FILE REFERENCE: B96-021-3
; CURRENT APPLICATION NUMBER: US/10/646,950
; CURRENT FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: 60/023,491
; PRIOR FILING DATE: 1996-08-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
;
; SEQ ID NO 3
; LENGTH: 2948
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1001)..(1945)

Query Match   8.2%; Score 30.5; DB 1; Length 2948;
Best Local Similarity 49.8%; Pred. No. 0;

Matches 102; Conservative 0; Mismatches 100; Indels 3; Gaps 1;

Qy   1 TTTGGAGTCGCGCCATTTCACCACATTATTGAGCAGCTGCGCTTCCGCCAGAGCAGTGTG 60
          ||||||||||| || ||| | || |||| ||||| |||||| ||||| ||| || ||||
Db 1568 TTTGGACTTGCGCGCACGCACCACCACCATGCTTATGAGCAATTACAGGAAGGCTTCAAACT 1627

Qy   61 GGAAGTACTTCGTTGCTGCAGCGGTTCCAGTTCTCTCCTACACCGCGTCGTCTTCGGGTG 120
          || || || ||||| | || |||| ||| ||||| |||||| | || | ||| |||
Db 1628 GTTTCCATTCTGCTGACAACACTGCTTCAAAATTTATACACAACACTTTTTGGAGGGTTA 1687

Qy 121 ACAGCTTTCCTCTTCATCCGCCACA---GGACACCTGATAGGGCGCCGGGTTCTCTGCCACTCT 177
          |||| ||||| || ||||| ||| | || |||| | || ||| || |
Db 1688 ACCAAGTTTGTATTCGTAAGAACAGGGCGGGAACCTATGGTGCTCGCATAATCCTGCATGCC 1747

Qy 178 TTCTGCAACTACACATGGGGCGTTCCCTG 202
          ||| |||| | |||| ||||| ||||||
Db 1748 CTTTGCAATATCATGGGGGTTTCCCTG 1772

RESULT 2
US-10-646-950-1
Sequence 1, Application US/10646950
; GENERAL INFORMATION:
; APPLICANT: Rine, Jasper
; APPLICANT: Boyartchuk, Victor L
; APPLICANT: Ashby, Matthew N
; TITLE OF INVENTION: AFC1 and RCE1: Isoprenylated CAAX Processing Enzymes
; FILE REFERENCE: B96-021-3
; CURRENT APPLICATION NUMBER: US/10/646,950
; CURRENT FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: 60/023,491
; PRIOR FILING DATE: 1996-08-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
;
; SEQ ID NO 1
; LENGTH: 1825
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (343)..(1701)

Query Match   4.4%; Score 16.4; DB 1; Length 1825;
Best Local Similarity 45.4%; Pred. No. 0;

Matches 59; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

Qy   98 ACACCGCTGTCTTCGGTGTCGGTCTTATACAGGTTTCCTCCATCCGCACAGGAGACACCTGATAG 157
          ||||| || | ||||| | | | |||| || | ||| || || || || |
Db 356 AGACGAATTCTGACACATCCTAATATCCCGTGGAAATTAATCATTTCTGGGGTTCTCGATTG 415

Qy 158 GGCCGGTTCTCTGCCACTCTTTTCTGCAACTACACATGGGGCTTCCCTGCCAGTGTGTTGCAGCC 217
          ||| || || |||| ||||| |||| || | || ||| |||||| |||| ||||
Db 416 CCCAATTTTCTTCGGAATCTTACTTGACGTTACAGACAGTACAGAAGCTATCTGAAACAA 475

Qy 218 TGGAGCATCC 227
          ||| |||||
Db 476 AGTTGCCACC 485

Search completed: April 18, 2006, 07:49:50
Job time : 1.01497 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 18, 2006, 07:49:48 ; Search time 0.985034 Seconds
                                            (without alignments)
                                            3.508 Million cell updates/sec

Title:
Perfect score: 358
Sequence: 1 cattattagccagatgaatt.........gagagacttcaagctttgaa 362

Scoring table: IDENTITY NUC
              Gapop 10.0 , Gapext 0.5

Searched: 2 seqs, 4773 residues

Total number of hits satisfying chosen parameters: 4

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 2 summaries

Database : US10646950_1_3.seq:*

                              SUMMARIES

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result   Query   %
No.   Score   Match Length DB   ID   Description
  1   33.7   9.4   1825 1   US-10-646-950-1   Sequence 1, Appli
c 2   24.4   6.8   2948 1   US-10-646-950-3   Sequence 3, Appli

                              ALIGNMENTS

RESULT 1
US-10-646-950-1 .
; Sequence 1, Application US/10646950
; GENERAL INFORMATION:
; APPLICANT: Rine, Jasper
; APPLICANT: Boyartchuk, Victor L
; APPLICANT: Ashby, Matthew N
; TITLE OF INVENTION: AFC1 and RCE1: Isoprenylated CAAX Processing Enzymes
; FILE REFERENCE: B96-021-3
; CURRENT APPLICATION NUMBER: US/10/646,950
; CURRENT FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: 60/023,491
; PRIOR FILING DATE: 1996-08-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
;
; SEQ ID NO 1
; LENGTH: 1825
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (343)..(1701)
US-10-646-950-1

Query Match   9.4%;   Score 33.7; DB 1; Length 1825;
Best Local Similarity   55.2%; Pred. No. 0;
Matches   85; Conservative   0; Mismatches 68; Indels   1; Gaps   1;

Qy   196 TGAGTTTCAAGCTGATGCAT-TGCCAAGAAACTTGGGAAGGCTAAAGACTTATATTCTGC 254
          ||||.||||||||||||||| ||||||||||.|||||||||||.||||||||||||||
Db   1509 TGAATATCAAGCTGATGCTTATGCTAAAAAAATTGGGCTACAAGCAAAAATCTATGTAGGGC 1568

Qy   255 TTTAATCAAAACTTAACAAAAGATAACTTGGGATTCCCTGTTTCTGACTGGTTGTTCTCAAT 314
          |||.||| |||||||||||||||||||||||||||||||||||||.||||||||||||||
Db   1569 TCTAATTGATCTACAAATCAAAATCAAAAACCTTTCCACCATGAAATGTAGATCCTCTGTATTCTTAG 1628

Qy   315 GTGGCATTATTCATCCTCCACTGCTAGAGAGA 348
          ||||||||||||||||||||||||||||||
Db   -- (alignment continues)

Db   1629 CTATCATTATTCCCATCCAACTTCCTAGCTGAAAGA 1662
          |||||||| ||||| ||| ||||||||||||||| ||| |||

RESULT 2
US-10-646-950-3/c .
; Sequence 3, Application US/10646950
; GENERAL INFORMATION:
; APPLICANT: Rine, Jasper
; APPLICANT: Boyartchuk, Victor L
; APPLICANT: Ashby, Matthew N
; TITLE OF INVENTION: AFC1 and RCE1: Isoprenylated CAAX Processing Enzymes
; FILE REFERENCE: B96-021-3
; CURRENT APPLICATION NUMBER: US/10/646,950
; CURRENT FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: 60/023,491
; PRIOR FILING DATE: 1996-08-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
;
; SEQ ID NO 3
; LENGTH: 2948
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1001)..(1945)
US-10-646-950-3

Query Match   6.8%;   Score 24.4; DB 1; Length 2948;
Best Local Similarity   46.7%; Pred. No. 0;
Matches   70; Conservative   0; Mismatches 80; Indels   0; Gaps   0;

Qy   27 TGTGTTTTTTTTTTATTTTGCTGTATTTAATTGGTCGGAAAAGGAGGACTTTTTGCTGCATTTGGTT 86
          |||||| | ||| ||| |||||||||||||||| ||||||||||||||||||||||||
Db   2862 TATATTTTGTAAAGTATCTTGTACAAGCCTCTAGGAAATTATCAGGCTTAACGTTAGGGTG 2803

Qy   87 TTTATGNTAGCCAACCCACTNTTATTGGGACTAATTGNTCATCCTCCAGTTTTATTTTTCAC 146
          ||| ||| ||| || |||| ||||||||||| ||| |||||||||||||||||| |||
Db   2802 TTGATTGGCGGGAACCCATAATAAGTTTTTCTTTAATACGTTAGCATTAATTCCTGGA 2743

Qy   147 CTTACAATGNGGTTCTTTCTTTTTTGCCTAA 176
          |||||||| |||||| ||||||||||
Db   2742 TGGAGAGTGAACACCTTTTTTTATACCTAA 2713

Search completed: April 18, 2006, 07:49:50
Job time : 0.985034 secs

```
OM protein - nucleic search, using frame_plus_p2n model

                              GenCore version 5.1.7
                         Copyright (c) 1993 - 2006 Biocceleration Ltd.

Run on:            April 18, 2006, 07:40:29 ; Search time 2.35938 Seconds
                                                (without alignments)
                                                2.115 Million cell updates/sec

Title:             US-10-646-950-2
Perfect score:     2342
Sequence:          1 MFDLKTILDHPNIPWKLIIS..........HPTLAERSTALLDYVSEKKKN 453

Scoring table:     BLOSUM62
                   Xgapext 10.0 ; Xgapext   0.5
                   Ygapop  10.0 ; Ygapext   0.5
                   Fgapop   6.0 ; Fgapext   7.0
                   Delop    6.0 ; Delext    7.0

Searched:          4 seqs, 5508 residues

Total number of hits satisfying chosen parameters:          8

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 4 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=soft -Q=US10646950.pep -DB=US10646950.seq
-SUFFIX=pto -OUT=align_p2n -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits
-START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=4 -DOCALIGN=200
-THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=4 -MODE=LOCAL -OUTFMT=pto
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -NCPU=6 -NO_XLPXY
-NEG_SCORES=0 -LONGLOG -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPOP=0.5 -DELOP=6 -DELEXT=7

Database :         US10646950.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                                  SUMMARIES

Result              %
No.    Score   Match  Length DB  ID                    Description
---    -----   -----  ------ --  --                    -----------
 1     2342    100.0   1825   1  US-10-646-950-1       Sequence 1, Appli
 2     194.5     8.3    362   1  US-10-646-950-6       Sequence 6, Appli
 3      64       2.7    373   1  US-10-646-950-5       Sequence 5, Appli
c4      61.5     2.6   2948   1  US-10-646-950-3       Sequence 3, Appli

                                 ALIGNMENTS

RESULT 1
US-10-646-950-1
; Sequence 1, Application US/10646950
; GENERAL INFORMATION:
;   APPLICANT: Rine, Jasper
;   APPLICANT: Boyartchuk, Victor L
;   APPLICANT: Ashby, Matthew N
;   TITLE OF INVENTION: AFC1 and RCE1: Isoprenylated CAAX Processing Enzymes
;   FILE REFERENCE: B96-021-3
;   CURRENT APPLICATION NUMBER: US/10/646,950
;   CURRENT FILING DATE: 2003-08-21
;   PRIOR APPLICATION NUMBER: 60/023,491
;   PRIOR FILING DATE: 1996-08-07
```

```
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin Ver. 2.1
;
; SEQ ID NO 1
;   LENGTH: 1825
;   TYPE: DNA
;   ORGANISM: Saccharomyces cerevisiae
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (343)..(1701)
; DB: US-10-646-950-1

US-10-646-950-2 (1-453) x US-10-646-950-1 (1-1825)

Alignment Scores:
Pred. No.:          1
Score:              5.22e-13
Score:              2342.00         Length:        1825
Percent Similarity: 100.0%          Matches:        453
Best Local Similarity: 100.0%       Mismatches:       0
Query Match:        100.0%          Conservative:     0
                                    Indels:           0
                    1               Gaps:             0

Qy    1 MetPheAspLeuLysThrIleLeuAspHisProAsnIleProTrpLysLeuIleIleSer 20
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  343 ATGTTTGATCTTAAGACGATTCTCGACCATCCTAATATCCCGTGGAAATTAATCATTTCT 402

Qy   21 GlyPheSerIleAlaGlnPheSerPheGluSerTyrLeuThrTyrArgGlnIleTyrGlyLys 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  403 GGGTTCTCGATTGCCCAATTTTCTTTCGAATCTTACTTGACGTACAGACAGTTCCAGAAG 462

Qy   41 LeuSerGluThrLysLeuValProProValLeuGluAspGluIleAspSerGluThrPheHis 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  463 CTATCTGAAACAAAAGTTGCCACCTGTCGTGGAAGACGAAAATGATGAGAAAACTTTTCAT 522

Qy   61 LysSerArgAsnTyrSerArgAlaLysAlaLysPheSerPheGlyAspValTyrAsn 80
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db  523 AAATCAAGGAACTACTCCCGGGCCAAGGCCAAGTTCTCCATTTCGGTGACGTCTATAAC 582

Qy   81 LeuAlaGlnLysLeuValPheIleLysSerTyrAspLeuPheProLysIleLeuTrpHisMetAla 100
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  583 CTAGCCCAAAAGCTAGTTTTCATCAAATACGACCTCTTCCCTAAAATCTTGGACATGGCC 642

Qy  101 ValSerValLeuAsnAlaValLeuProValArgPheHisMetValSerThrValAlaGln 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  643 GTTTCTGTTCTTAATGCAGTCCTGCCAGTCAGATTCATATGGTCACCGTCGCACAG 702

Qy  121 SerLeuCysPheLeuGlyLeuLeuSerSerLeuSerThrLeuValAspLeuProLeuSer 140
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db  703 AGTTTATGCTTCTTGGGTCTCTTATCCAGTTTGCTACCTTGGTTGATTTGCCACTCTCT 762

Qy  141 TyrTyrTyrSerHisPheValLeuGlyLysLysPheGlyPheAsnLysLeuThrValGlnLeu 160
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db  763 TACTATAGGCCATTTTGTCCTGGAAAAAATTTGGTTTCAATAAAATTGACCGGTCCAACTA 822

Qy  161 TrpIleThrAspMetIleLysSerLeuArgThrIleLeuAlaIleGlyGlyProIleLeu 180
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db  823 TGGATCACCGATATGATCAAGAGTCTGAGACTTTGGGGTATCGGTGGGCCCAAATCCTT 882

Qy  181 TyrLeuPheLeuLysIlePheAspGlysPheProThrAspPheLeuTrpTyrIleMetVal 200
          |||||||||||||||||||||||||||||||||||||||||||||
Db  883 TACCTGTTCCTTAAGATCTTTGATAAATTCCCTACTGATTTCCTTTGGTACATTATGGTC 942

Qy  201 PheLeuPheValValGlnIleLeuLeuAlaMetThrIleIleProValPheIleMetProMet 220
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db  943 TTCTTGTTCGTTGTCCAAAATCTTAGCCATGACAAATCATTCCAGTCTTCATCATGCCCATG 1002

Qy  221 PheAsnLysPheThrProLeuGluAspGlyValGluLeuLysSerGluSerLeuAla 240
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db 1003 TTTAATAAAGTTCACTCCATTGGAGGACGGGTGAACTGAAAAATCTATTGAAAAGTTGGCC 1062

Qy  241 AspArgValGlyPheProLeuAspGlyIleIlePheValIleAspGlySerLysArgSerSer 260
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db 1063 GATAGAGGTTGGGTTCCCTCTAGATAAGATTTTTGTCATTGACGGGCTCAAAAAGATCTTCT 1122
```

```
Qy   261 HisSerAsnAlaTyrPheThrGlyLeuProPheThrSerLeuValLeuPheAsp      280
Db  1123 CATTCAAACGGCATATTCACAGAGTTTGCCATTCACCTCAAAGAGAATTGTTTCTTGTTGAC  1182

Qy   281 ThrLeuValAsnSerAsnSerThrAsnAspGluIleThrAlaValLeuAlaHisGluIleGly  300
Db  1183 ACTTTAGTGAACAGTAATTCTACTGATGAAAATTACGGCGTGTTTGGCCATGAAATGGT      1242

Qy   301 HisTrpGlnLysAsnHisIleValIleAsnMetValIlePheSerGlnLeuHisThrPheLeu  320
Db  1243 CACTGGCAAAAAAACCACATCGTTAATATGGTCATCTTTAGTCAAATTGCACACCTTCTC      1302

Qy   321 IlePheSerLeuPheThrSerIleTyrArgAsnThrSerPheThrTyrAsnThrPheGlyPhe  340
Db  1303 ATTTTCTCCCTTTTCACCAGCACTCTACAGAAATACATCATTTACAACACCTTCGGCTTT      1362

Qy   341 PheLeuGlyLysSerThrGlySerPheValAspProValIleThrLysGluPheProIle     360
Db  1363 TTCTTAGGAAAGTCCACTGGCAGTTTTGTTGATCCGGTTATCACTAAGGAATTCCCCATT      1422

Qy   361 IleIleGlyPheMetLeuPheAsnAspLeuLeuThrProLeuGluCysAlaMetGlnPhe     380
Db  1423 ATCATTGGATTTATGTTATTTAACGACTTATTAACTCCACTCGAATGTGCCATGCAATTC      1482

Qy   381 ValMetSerLeuLeuIleSerArgThrHisGluTyrGlnAlaAspAlaTyrAlaLeuLysSerLeu  400
Db  1483 GTGATGAGTTTATTAATTTCCAGAAATCCATGAAATATCAAGCTGATGCTTATGCTAAAATTG    1542

Qy   401 GlyTyrTyrLysGlnAsnLeuCysSerArgAlaLeuLeuIleAspLeuGlnIleIleLysAsnLeuSerThr  420
Db  1543 GGCTACAAGCAAAATCTATGTAGGGCTCTAATTGATCTACAAAATAAAAACCTTTCCACC      1602

Qy   421 MetAsnValAlaSerProLeuTyrSerSerTyrHisTyrSerHisProThrLeuAlaGluArg   440
Db  1603 ATGAATGTAGCATCCCTGTATTCTAGCTATCATTATTCCCATCCAAACTCTAGCTGAAAGA     1662

Qy   441 SerThrArgAlaLeuAspTyrValSerGluLysLysLysLysAsn      453
Db  1663 TCGACCGCTCTAGACTATGTTAGTGAAAAGAAAAAAAAC             1701
```

RESULT 2
US-10-646-950-6
Sequence 6, Application US/10646950

US-10-646-950-6

```
Alignment Scores:
Pred. No.:
Score:                      194.50
Percent Similarity:          52.2%        Length:          362
Percent Identity:                         Matches:          49
Best Local Similarity:       36.6%        Conservative:     21
Query Match:                  8.3%        Mismatches:       49
                                          Indels:           16
                                          Gaps:              2
```

US-10-646-950-2 (1-453) x US-10-646-950-6 (1-362)

```
Qy   312 IlePheSerGlnLeuHisThrPheLeuIlePheSerLeuPheThrSerIleTyrArgAsn     331
         |||||||| :::|||||||   ||||||    |||||
Db     2 ATTATTAGCCAGATGAAATTCTTCCTGTGTTTTTTTTTATTTGCTGTATTAATTGGTCGA      61

Qy   332 ThrSerPheThrTyrAsnThrPheGlyPhePheLeuGlyLysSerThrGlySerPheValAsp   351
         :::                         ::::::
Db    62 AAGGAGGCTTTTGCTGCATTTGGTTTTTATGTNTAGNTAGCCAA                     100

Qy   352 ProValIleThrLysGluPheProIleIleIleGlyPheMet---LeuPheAsnAspLeu      370
                    :::                         :::::  LeuPheAsnAspLeu
Db   101 ----------CCCACTNTTATTGGACTATTGNTCAATCTTCAGTTTATT                139

Qy   371 LeuThrProLeuGluCysAlaMetGlnPheValMetSerLeuLeuIleSerArgThrHisGlu   390
                |||      :::           :::            |||
Db   140 TTTTCACCTTACAAATGNNGGGTTCTTTTCTTTTTTGGCCTAACAGTGCCTAACAGCGCC      199

Qy   391 TyrGlnAlaAspAlaTyrAlaLeuLysLeuGlyTyrTyrLysGlnAsnLeuCysSerArgAlaLeu  410
         :::||| |||:::            :::||||        :::|||||
Db   200 TTTCAAGCTGATGCATT-GCCAAGAAACTTGGGAGGCTAAAGACTTATATTCTGCTTA        258

Qy   411 IleAspLeuGlnIleIleLysAsnLeuSerThrMetAsnValAlaSerProLeuTyrSerSerTyr  430
         |||:::|||     :::  |||:::   |||      ||||||
Db   259 ATCAAACTTAACAAAGATAACTTGGGATTCCCGTTTTCTGACTGGTTGTTTCTCAATGTGG    318

Qy   431 HisTyrSerHisProThrLeuAlaGluArgSerThrArgAlaLeu                    444
         ||| |||        :::||| ||||||
Db   319 CATTATTCTCATCCTCCACACGCTCTAGAGGAGACTTCAAGCTTG                    360
```

RESULT 3
US-10-646-950-5
Sequence 5, Application US/10646950

US-10-646-950-5

```
Alignment Scores:
Pred. No.:                   2.89
Score:                      64.00
Percent Similarity:          40.5%        Length:          373
Percent Identity:            25.3%        Matches:          20
Best Local Similarity:        2.7%        Conservative:     12
Query Match:                              Mismatches:       37
                                          Indels:           10
                                          Gaps:              2
```

US-10-646-950-2 (1-453) x US-10-646-950-5 (1-373)

```
Qy   299 IleGlyHisTrpGlnLysAsnHisIleValAsnMetValIlePheSerGlnLeuHisThr    318
         :::  ||||||||    :::|||||
Db     7 GTCGCCCATTTT-----CACCAATATTATTGAGCAGCTGCGCTTCCGCCAGAGCAGTGTG    60

Qy   319 PheLeuIlePheSerLeuPheThrSerIleTyrArgAsnThrSerPheThrTyrAsnThrPhe  338
         :::|||     |||:::
Db    61 GGAAGTATCTTCGGTGTGTCTGCAGGCGTTCCAGTTCTCTACACCGCTCTCTTCGGTGTTAT  120

Qy   339 GlyPhePheLeuGlyLysSerThrGlySerPheValAspProValIleThrLysGluPhe    358
         ||||||               :::
Db   121 ACAGCTTTCCTCTTCCTCATCCGGCACAGGACACCTGTTCTCTGCCACTCTTC          180
```

```
Qy    359  ProIleIleGlyPheMetLeuPheAsnAspLeuLeuThrProLeuGluCysAla  377
                :::||||
Db    181  TGCAACTACATGGGCTTC--------------------CCTGCAGTGTGTGCA  213

RESULT 4
US-10-646-950-3/c
; Sequence 3, Application US/10646950
; GENERAL INFORMATION:
; APPLICANT: Rine, Jasper
; APPLICANT: Boyartchuk, Victor L
; APPLICANT: Ashby, Matthew N
; TITLE OF INVENTION: AFC1 and RCE1: Isoprenylated CAAX Processing Enzymes
; FILE REFERENCE: B96-021-3
; CURRENT APPLICATION NUMBER: US/10/646,950
; CURRENT FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: 60/023,491
; PRIOR FILING DATE: 1996-08-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1001)..(1945)
US-10-646-950-3
  LENGTH: 2948
  TYPE: DNA
  ORGANISM: Saccharomyces cerevisiae

Alignment Scores:
Pred. No.:
Score:                 2.96
Percent Similarity:    61.50
Best Local Similarity: 38.2%
Query Match:           20.9%
                        2.6%
                        1

                       Length:       2948
                       Matches:       68
                       Conservative:  56
                       Mismatches:   108
                       Indel:         93
                       Gaps:          15
```

```
US-10-646-950-2 (1-453) x US-10-646-950-3 (1-2948)

Qy    18  IleIleSerGlyPheSerIleAlaGlnPheSerGluSerTyrLeuThr-TyrArgGl  37
              ||:|||  ||
Db   860  ATCATCAAAGGTTTTCCATCCAGTGGTCCAAAAAAAAATACAGAGCAACAAAAGA  801

Qy    37  nTyrGlnLysGluThrLysProProValLeu-------GluAspGluIl  54
              :::||||||||:::
Db   800  GCACCAGAAAATGCATTTAAAAGAATTTATTAATAATAGGGAATACAAAGACCGCGAT  741

Qy    54  eAsp---------------------AspGluThrPheHisLysSer--  67
              |:::                       ||:|
Db   740  AAATACCTTCATCTATTAAGCAACCATACATTATATCTATATAAGAAAAGTAACGAG  681

Qy    67  gAlaLysAlaLysPheSerIlePheGlyAspValTyr------------  79
              |||||||                             :::
Db   680  A----------------ATTTTTCTAAGTTTTTTATTTGTTCACTTGCCTAACAG  639

Qy    80  --------AsnLeuAlaGlnLysLeuValPheIleLysTyrAspLeuPhePro--  94
                      |||||||
Db    ...  --AACTTCAAGTTCACATTAAGTCTCGTTTG--  474

Qy   104  uAsnAlaValLeuProValArgPheHis-MetValSerThrValAlaGlnSerLeuCysP  124
              ||||                 :::                    |||
Db   524  TAAATGTCTTATTAAATTCCAAAGTTCACATTAAGTCTCGTTTG--  474

Qy   124  heLeuGlyLeuLeuSerSerLeuSerThrLeu---------------ValAsp-  136
              :::|||||||                              |||
Db   473  AAGGAGCAAACCTACCCCATTTATGAACAAATCTGGTCTGTAAATTTCAGGGAGAAGTAGACG  414

Qy   137  --LeuProLeuSerTyrTyrSerHisPheValLeuGluGluLysPheGlyPheAsnLysL  156
              :::                  |||
Db   413  AGCTACCGGCTAGGTAAAAATAAACTACTCTTGGATGAAGAGTTACTGGCGTTAATGACG  354

Qy   353  CTGAACTGGGCGACGATGAACTACCGTTACCCTGTGTGCCATAT  294
              :::      ||||||||
Db   156  eu----------------------ThrValGlnLeuTrpIleThrAspMetIleLysSerLeuThrL  171

Qy   293  CCGTGCTTTGAGTGTGTTGTTTTAGGTACTGACCTGTGTTTTTAAAAAGTTGGATAAGTTGT  234
              :::||||        |||::::
Db   171  euAlaTyrAlaIleGlyProIleLeuTyrIleLeuPheLeuLysIlePheAspPhePheP  191

Qy   233  GAACA----------------------CTAACTTCAAGTTGCAAATGCTTTCGATAT  198
              |||
Db   191  roThrAspPhePheLeuTrpTyrIleMetValPheLeuProValValGlnIleIleLeuAlaMetT  211

Qy   211  hrIleIleProValPheIleMetProMetPheAsnLysPheProLeuGluGluGlyGlyG  231
              :::
Db   197  CG---------------------------TTAAACAGCTGTG  183

Qy   182  AAGTAATAAAATCTGTAAAATTCAGTTCCTTGGCCTACAGCGGTTCTCCCCTA------T  132
              :::||||
Db   231  lnLeuLysSerIleGluSerLeuAlaAspArgValGlyPheProLeuAspLysIleP  251

Qy   131  TCATATTATATAACTCATTAATTCAAGAAAATTCTTGTTGAACTTGGTTTCATAATTCAC  72
              |||
Db   263  snAlaTyrPheThrGlyLeuProPheThrSerLysArgIleValLeuPheAspThrLeuV  283

Qy    71  AAATTTTTGAATTGGAAAATCATCCTACAAAAGCTTTGATCGTTGTTCAGCTTCTTCTTTTGTTCA  12
              :::||||                    :::||
Db   283  alAsnSerAsn  286

Qy    11  TCAACAGTTCA  1
              |||||||||:::
Db   286  alAsnSerAsn
```

```
Searched:        4 seqs, 5508 residues

Total number of hits satisfying chosen parameters:   8

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 4 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=soft -Q=US10646950.pep -DB=US10646950.seq
-SUFFIX=pto -OUT=align_p2n -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits
-START=-1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=4 -DOCALIGN=200
-THR_SCORB=pct -THR MAX=100 -THR_MIN=0 -ALIGN=4 -MODB=LOCAL -OUTFMT=pto
```

```
Scoring table:      BLOSUM62
                    Xgapop   10.0 ,  Xgapext   0.5
                    Ygapop   10.0 ,  Ygapext   0.5
                    Fgapop    6.0 ,  Fgapext   7.0
                    Delop     6.0 ,  Delext    7.0

Title:            US-10-646-950-4
Perfect score:    1651
Sequence:         1 MLQFSTFLVLILYISISYVLP..........ISLKDTLQTLVGTPGYRITL 315

Run on:           April 18, 2006, 07:40:29 ;  Search time 1.64062 Seconds
                                              (without alignments)
                                              2.115 Million cell updates/sec

OM protein - nucleic search, using frame_plus_p2n model

Copyright (c) 1993 - 2006  Bioacceleration Ltd.

                          GenCore version 5.1.7

Search completed: April 18, 2006, 07:40:35
Job time : 4.35938 secs
```

-NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -NCPU=6 -NO_XLPXY
-NBG_SCORES=0 -LONGLOG -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

US10646950.seq:*

Pred. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	% Length	DB	ID	Description
1	1651	100.0	2948	1	US-10-646-950-3	Sequence 3, Appli
2	163	9.9	373	1	US-10-646-950-5	Sequence 5, Appli
3	54	3.3	1825	1	US-10-646-950-1	Sequence 1, Appli
4	43.5	2.6	2948	1	US-10-646-950-3	Sequence 3, Appli

c 4

ALIGNMENTS

RESULT 1
US-10-646-950-3
Sequence 3, Application US/10646950
GENERAL INFORMATION:
APPLICANT: Rine, Jasper
APPLICANT: Boyartchuk, Victor L
APPLICANT: Ashby, Matthew N
TITLE OF INVENTION: AFC1 and RCE1: Isoprenylated CAAX Processing Enzymes
FILE REFERENCE: B96-021-3
CURRENT APPLICATION NUMBER: US/10/646,950
CURRENT FILING DATE: 2003-08-21
PRIOR APPLICATION NUMBER: 60/023,491
PRIOR FILING DATE: 1996-08-07
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3
LENGTH: 2948
TYPE: DNA
ORGANISM: Saccharomyces cerevisiae
FEATURE:
NAME/KEY: CDS
LOCATION: (1001)..(1945)

US-10-646-950-3

Alignment Scores:
Pred. No.:   3.08e-09
Score: 1651.00
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
DB: 1

US-10-646-950-4 (1-315) x US-10-646-950-3 (1-2948)

```
Qy      1 MetLeuGlnPheSerThrPheLeuValLeuTyrIleSerTyrValLeuPro 20
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1001 ATGCTACAAATTCTCAAACATTTCTAGTGTCCTATACATCTCTATGTGCTACCTCCG 1060

Qy     21 LeuTyrArgAlaThrSerGlnProGluGlySerLysArgArgAspAsnProArgThrIleLysSer 40
            |||||||||||||||||||||||||||||||||||||||||||||
Db   1061 CTATATGCAACTTCACACACCAGAAGGGGTCTAAACGAGATAAATCCTCGAACGATTAAATCT 1120

Qy     41 ArgMetGlnLysLeuThrIleMetLeuIleSerAsnLeuPheLeuValProPheLeuGln 60
            |||||||||||||||||||||||||||||||||||||||
Db   1121 CGGATGCAAAAACTTAACAATTAATGCTAATTTCAACCTTTTTGGTGCCTTTTTACAA 1180

Qy     61 SerGlnLeuSerSerThrHisIleSerPheLysAspAlaPheLeuGlyLeuGly 80
            |||||||||||||||||||||||||||||||||||||||||||
Db   1181 TCTCAATTAATTCTAGTACCACACTTCACATATAAGTTTCAAGGACGGCAATTTTTAGGCTTAGGT 1240
```

RESULT 2
US-10-646-950-5
Sequence 5, Application US/10646950
GENERAL INFORMATION:
APPLICANT: Rine, Jasper
APPLICANT: Boyartchuk, Victor L
APPLICANT: Ashby, Matthew N
TITLE OF INVENTION: AFC1 and RCE1: Isoprenylated CAAX Processing Enzymes
FILE REFERENCE: B96-021-3
CURRENT APPLICATION NUMBER: US/10/646,950
CURRENT FILING DATE: 2003-08-21
PRIOR APPLICATION NUMBER: 60/023,491
PRIOR FILING DATE: 1996-08-07
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 5
LENGTH: 373
TYPE: DNA
ORGANISM: mouse
US-10-646-950-5

Alignment Scores:
Pred. No.:   0.831
Score: 163.00
Percent Similarity: 54.5%

```
Qy     81 IleIleProGlyTyrTyrAlaAlaIleLeuProAsnProTrpGlnPheSerGlnPheValLys 100
            ||||||||||||||||||||||||||||||||||||||||||||
Db   1241 ATTATCCCAGGTTATTACGCTGCAATTCTGCCAAACCCCTTGGCAAATTCGTCAGCCAGTTCGTCGAA 1300

Qy    101 AspLeuThrLysCysValAlaAlaMetLeuLeuThrLeuTyrCysGlyProValLeuAspPhe 120
            |||||||||||||||||||||||||||||||||||||||||||||
Db   1301 GACTTAACGAAATGTGTTGCGGCAATGTTATTGACCTTATATTGTGGACCCGTTTTAGATTTT 1360

Qy    121 ValLeuTyrHisLeuLeuAsnProLysSerSerIleLeuGluAspPheTyrHisGluPhe 140
            ||||||||||||||||||||||||||||||||||||||||||||
Db   1361 GTATTATATCATTTATTAAATCCAAAGAGCTCTATACTTGAAGATTTTTACCATGAATTC 1420

Qy    141 LeuAsnIleTrpSerPheArgAsnPheIlePheGlnIleThrGluGlnIlePheTyr 160
            ||||||||||||||||||||||||||||||||||||||||||
Db   1421 CTGAATATTTGGAGTTTCAGGAATTTTATATTTGCACCAATAACTGAAGGAAAATATTTTAC 1480

Qy    161 ThrSerMetLeuLeuThrThrTyrLeuAsnLeuIleProHisSerGlnLeuSerTyrGln 180
            |||||||||||||||||||||||||||||||||||||||||||
Db   1481 ACGTCAATGCTTTTGACTACGTACTTAAACTAATACCGCATTCGCAACTAAGCTATCAA 1540

Qy    181 GlnLeuPheTrpGlnProSerLeuPhePheGlyLeuAlaHisAlaHisHisAlaTyrGlu 200
            ||||||||||||||||||||||||||||||||||||||||||||
Db   1541 CAGTTATTTTGGCAACCATCGCTTTTTTTTGGACTTGCGGCACGCACCCATGCTTATGAG 1600

Qy    201 GlnLeuGlnGluGlySerMetThrThrValSerIleLeuLeuLeuThrThrCysPheGlnIle 220
            |||||||||||||||||||||||||||||||||||||||||||||
Db   1601 CAATTACAGGAAGGGTCCATGACAACTGTTTCCATTCTGCTGACAACATGTTTCCAAAATT 1660

Qy    221 LeuTyrThrThrLeuPheGlyLeuGluThrLysPheValPheValArgThrGlyGlyAsn 240
            ||||||||||||||||||||||||||||||||||||||||||||
Db   1661 TTATACACAACACTTTTTGGAGGGGTTAACCAAGTTTGTATTCGTAAGAACAGGCGCGGAAC 1720

Qy    241 LeuTrpProCysSerIleIleLeuHisIleAlaLeuCysAsnIleMetGlyPheProGlyProSer 260
            |||||||||||||||||||||||||||||||||||||||||||||
Db   1721 CTATGGGTGCTGCATAATTCCTGCATGCCCTTTGCAAATATCATGGGGTTTCCTGGTCCTTCA 1780

Qy    261 ArgLeuAsnLeuHisPheThrValAlaAspLysLysAlaGlyArgIleSerLysLeuVal 280
            |||||||||||||||||||||||||||||||||||||||||||
Db   1781 AGATTGAAATTACATTTCACAGTAGCAGACAAGAAAGCTGGACGCGGATTTCCAAAATGGTC 1840

Qy    281 SerIleLeuTrpAsnLysCysTyrPheAlaLeuLeuLeuValLeuGlyLeuLeuSerLeuLysSerAsp 300
            |||||||||||||||||||||||||||||||||||||||||||||
Db   1841 TCAAATCTGGAATAAGTGCTACTTCGCACTCGTCCTTGGATTAATATCCCTGAAGGAT 1900

Qy    301 ThrLeuGlnThrLeuValGlyThrProGlyTyrTyrArgIleThrLeu 315
            |||||||||||||||||||||||||||||||||||||||||
Db   1901 ACCTTACAAAACTCTGGTAGGAAACTCCCTGGTTTATAGAATAAACCCTT 1945
```

Alignment Scores:
Length: 373
Matches: 36
Conservative: 18

Length: 2948
Matches: 315
Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0